

<110> Braun, Jonathan
Sutton, Christopher L.

<130> P-PM 4966

<150> US 09/303,120

<151> 1999-04-30

<150> US 09/820,576

<151> 2001-03-28

<160> 10

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 302

<212> DNA

<213> Unknown

$\langle 220 \rangle$

<223> Microbial Organism from the human gut

<221> CDS

 $\langle 222 \rangle \quad (2) \dots (301)$

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a gat (ctg gcc agc) gcc (gtg ggc atc) (cag) tcc (ggc agc atc) ttt cat cac 49
Asp Leu Ala Ser Ala Val Gly Ile Gln Ser Gly Ser Ile Phe His His
1 5 10 15

(ttc) (aag) (agc) (aag) (gat) (gag) ata ttg cgt gcc gtg atg gag gaa acc atc 97
 Phe Lys Ser Lys Asp Glu Ile Leu Arg Ala Val Met Glu Glu Thr Ile
 8 20 25 30

cat tac aac acc gcg atg atg cgc gct tca ctg gag gag gcg agc acg 145
His Tyr Asn Thr Ala Met Met Arg Ala Ser Leu Glu Glu Ala Ser Thr
35 40 45

gtg cgc gaa cgc gtg ctg gcg ctg atc cgc tgc gag ttg cag tcg atc 193
Val Arg Glu Arg Val Leu Ala Leu Ile Arg Cys Glu Leu Gln Ser Ile
50 55 / 60

atg ggc ggc agt ggc gag gcc (atg gcg gtc) (ctg gtc) tac gaa tgg cgc 241
Met Gly Gly Ser Gly Glu Ala Met Ala Val Leu Val Tyr Glu Trp Arg
65 70 75 80

↑

5

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<400> 3
a gat ctt gag cgt cat gag tgc ctg ggg tac gcc ttt tca tgc cgt ccg 49
  Asp Leu Glu Arg His Glu Cys Leu Gly Tyr Ala Phe Ser Ser Arg Pro
    1             5             10             15
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SECRET

gcg gat cga gag tgg gtg ttt ttt cag ggc acg gtt tcc tac aag gta 97
Ala Asp Arg Glu Trp Val Phe Phe Gln Gly Thr Val Ser Tyr Lys Val
20 25 30

cga gtg gcc agc cgt ttg ctc atc aat gaa agc cgg gca ttg atg tcg 145
Arg Val Ala Ser Arg Leu Leu Ile Asn Glu Ser Arg Ala Leu Met Ser
35 40 45

gcg gca ttg gat ggt ttt ggc ata gtg ctc ggc ccg caa gac ttc ctg 193
Ala Ala Leu Asp Gly Phe Gly Ile Val Leu Gly Pro Gln Asp Phe Leu
50 55 60

cga acg gcg ttg gcg agt ggc gag ttg gtg cgg gtg ttg ccg gag ttt 241
Arg Thr Ala Leu Ala Ser Gly Glu Leu Val Arg Val Leu Pro Glu Phe
65 70 75 80

gag gct ccg agt cgg tcg atg cat ttg gtc tac acc gca aac cgc cag 289
Glu Ala Pro Ser Arg Ser Met His Leu Val Tyr Thr Ala Asn Arg Gln
85 90 95

cgt acc gcc aag ttg cgc tgc ttt gtc gag act gtg ctg gga cgt ttt 337
Arg Thr Ala Lys Leu Arg Cys Phe Val Glu Thr Val Leu Gly Arg Phe
100 105 110

ggt ccg gta tgaaggagca ccaccgtggc ggtcgccggg angcacctaa 386
Gly Pro Val
115

agatct 392

<210> 4
<211> 115
<212> PRT
<213> Unknown

<220>
<223> Microbial organism from the human gut

<400> 4
Asp Leu Glu Arg His Glu Cys Leu Gly Tyr Ala Phe Ser Ser Arg Pro
1 5 10 15
Ala Asp Arg Glu Trp Val Phe Phe Gln Gly Thr Val Ser Tyr Lys Val
20 25 30
Arg Val Ala Ser Arg Leu Leu Ile Asn Glu Ser Arg Ala Leu Met Ser
35 40 45
Ala Ala Leu Asp Gly Phe Gly Ile Val Leu Gly Pro Gln Asp Phe Leu
50 55 60
Arg Thr Ala Leu Ala Ser Gly Glu Leu Val Arg Val Leu Pro Glu Phe
65 70 75 80
Glu Ala Pro Ser Arg Ser Met His Leu Val Tyr Thr Ala Asn Arg Gln
85 90 95
Arg Thr Ala Lys Leu Arg Cys Phe Val Glu Thr Val Leu Gly Arg Phe

0996608-092701

Gly Pro Val 100 105 110
115

<210> 5
<211> 114
<212> PRT
<213> Unknown

<220>
<223> Microbial Organism from the human gut

<221> VARIANT
<222> (1)...(114)
<223> Xaa = Any Amino Acid

<400> 5
Arg Thr Arg Arg Ile Ser Leu Pro His Lys Lys Leu Ala Arg Asn Gly
1 5 10 15
Val Leu Tyr Ser His Gly Ala Thr Gln Glu Asp Ile Phe Ala Pro Cys
20 25 30
Gln His Arg Arg Cys Gln Ile Thr Lys Ala Tyr His Glu Ala Arg Leu
35 40 45
Val Glu Gln Ser Arg Arg Gln Arg Thr Ala Leu Gln His Pro His Gln
50 55 60
Arg Leu Lys Leu Ser Arg Thr Pro Arg His Met Gln Asp Val Gly Cys
65 70 75 80
Val Ala Leu Thr Gly Gly Leu Gln Ala Ala Lys Asp Leu Ser His Gln
85 90 95
Ser Thr Lys Thr Arg Tyr Ser Pro Ala Gly Gly His Arg Asp Gly Pro
100 105 110
Xaa Val

<210> 6
<211> 190
<212> PRT
<213> Clostridium pasteurianum

<400> 6
Met Asn Lys Thr Lys Asp Asn Ile Phe Tyr Ser Ala Ile Lys Val Phe
1 5 10 15
Ser Asn Asn Gly Tyr Asn Gly Ala Thr Met Asp Glu Ile Ala Ser Asn
20 25 30
Ala Gly Val Ala Lys Gly Thr Leu Tyr Tyr His Phe Lys Ser Lys Glu
35 40 45
Glu Ile Phe Lys Tyr Ile Ile Glu Glu Gly Val Asn Leu Met Lys Asn
50 55 60
Glu Ile Asp Glu Ala Thr Asp Lys Glu Lys Thr Ala Leu Glu Lys Leu
65 70 75 80
Lys Ala Val Cys Arg Val Gln Leu Asn Leu Ile Tyr Lys Asn Arg Asp

FD-250 (Rev. 10-6-60)

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<210> 7
<211> 200
<212> PRT
<213> Mycobacterium tuberculosis
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<210> 8
<211> 192
<212> PRT
<213> Auifex aeolicus
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<400> 8
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 1 5 10 15
 Lys Ile Leu Ser Ser Ala Leu Lys Leu Phe Ser Lys Lys Gly Phe Lys
 20 25 30
 Glu Thr Thr Ile Lys Asp Ile Ala Lys Glu Val Gly Ile Thr Glu Gly
 35 40 45
 Ala Ile Tyr Arg His Phe Thr Ser Lys Glu Glu Ile Ile Lys Ser Leu
 50 55 60
 Leu Glu Ser Ile Thr Lys Glu Leu Arg His Lys Leu Glu Val Ala Leu
 65 70 75 80
 Gln Arg Gly Glu Thr Asp Glu Glu Ile Leu Glu Ser Ile Val Asp Thr
 85 90 95
 Leu Ile Asp Tyr Ala Phe Ser Asn Pro Glu Ser Phe Arg Phe Leu Asn
 100 105 110
 Leu Tyr His Leu Leu Lys Glu Tyr Gly Glu Val Lys Asn Leu Pro Gly
 115 120 125
 Glu Leu Ile Leu Lys Phe Leu Asn Gly Leu Tyr Leu Lys Arg Lys Leu
 130 135 140
 Lys Thr Tyr Pro Glu Ile Ala Leu Ala Val Val Thr Gly Ser Val Glu
 145 150 155 160
 Arg Val Phe Ile Phe Lys Glu Arg Asn Phe Leu Asp Tyr Asp Glu Glu
 165 170 175
 Thr Ile Lys Lys Glu Leu Lys Lys Val Leu Lys Ser Ala Ile Leu Ala
 180 185 190

<210> 9
 <211> 18
 <212> DNA
 <213> Unknown
 <220>
 <223> Microbial Organism from the human gut

<400> 9
 ccgtgggcat ccagtcgcg 18

<210> 10
 <211> 19
 <212> DNA
 <213> Unknown

<220>
 <223> Microbial Organism from the human gut

<400> 10
 tctgctcata cacgtcacg 19

00996600-09996600